



The effects of four selected synbiotics on community and activity of the intestinal microbiota using a simulated colon model

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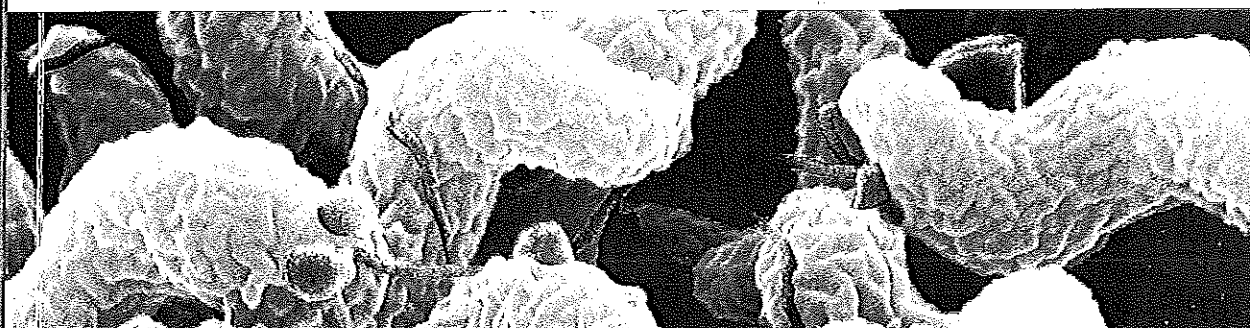
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Uyttendaele Mieke	PEC2.33	van Niel EWJ	PEB1.16	Vilu R	PEC1.24	
	PEC2.34	van Niel, Ed	PSE2.01	Vincent T	PEB2.20	
	PED1.24	* van Zanten Gabriella	PEE2.24	Vinderola GC	PEE2.08	
PSB1.01, PSC1.05, PSD1.01, PSC2.04		van Zuijlen, A	PSC2.01	Vinicius Ferreira de, M	PSA1.04	
Vadalà C	PEA1.54	Vanamayya PR	PEB1.17	Vinjé J	PEC1.57	
Valarelli LTV	PEA1.28	Vandenberg, O	PSC1.05	Vio P	PEC2.39	
Valdramidis V	PEC1.63	Vanderkelen L	PEB1.33	Virtanen, Sonja	PSD1.02	
Valdramidis Vasilis	PED2.37	Vanlint D	PEB2.66	Viviana C	PEA1.34	
Valero A	PEC2.60	Vannini L	PEA2.43	Vlaemyneck G	PEC1.25	
Valero Antonio	PEC1.05	Vannini Lucia	PEB2.67	Vlaemyneck G	PED1.26	
Valero Antonio	PEC2.02		PED2.17	Vlkova E	PEE2.17	
Valery S	PEC2.43	Vasudevan Gowthaman	PEB1.17	Vlkova Eva	PEE2.23	
Valik Lubomir	PEC1.04	Vauterin L	PEC1.47		PED2.55	
Valik U	PEC1.15	Vauterin P	PEC1.47	Vogensen FiK	PEE2.14	
Valik U	PEC1.16	Vaz F	PEB2.04		PEA1.17	
Valik U	PEC1.14	Vega E	PEC1.57		PSE1.03	
van Beilen J	PEB2.04	Vega Y León Salvador	PEC2.38	Vorster R	PEC1.06	
van Belkum, A	PSC1.05	Velasco R	PEC1.90	Voysey Philip	PEB2.44	
Van Boeijen Ineke KH	PEC1.29	Velliou E	PEC2.56		PED1.30	
Van Brandt L	PED1.26	Velliou Eirini	PEC1.94	Vrancken G	PEA1.21	
Van Bree I	PEA2.11	Venketash G	PEB1.17	Wacheck S	PEB1.14	
Van Camp J	PEA2.47	Venter P	PEA1.49	Wacheck S	PED1.15	
Van Coillie E	PEA2.31	Venter P	PEA2.07	Wacheck Silke	PED1.11	
	PEC1.25	Venter Pierre	PEB1.22	Wacher Carmen	PEA1.12	
	PEC1.58	Vercammen, Anne	PSD2.05	Wagner M	PEC1.95	
	PEC2.15	Verhaelen Katharina	PED2.56		PEC1.98	
	PEC2.48	Vermeulen A	PEC1.94		PEC1.99	
	PED1.26	Vermeulen An	PEC1.46		PEB2.32	
van Coillie Els	PEC1.91	Vermeulen, A	PSB1.01,		PEC2.06	
	PSB1.01	Vernocchi P	PEA2.43	Wakushima M	PEB1.02	
Van Damme I	PEC1.69	Vernocchi Pamela	PED2.58	Walcher G	PEC1.98	
Van de Vorst J	PED1.24	Vernocchi, P	PSA2.04,	Walcher Georg	PEC1.95	
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van der Merwe Enette	PEA2.07	Verran J	PED2.16	Wallin Carlquist Nina	PEB1.04	
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Van Derlinden E	PEC1.63		PEC1.59	Walton Gemma E	PEE2.25	
	PEC1.94		PEC1.60	Wang Lili	PEB1.02	
	PEC2.56		PEC1.61	Wang, Y	PSA2.06	
Van Derlinden Eva	PEC1.85	Vidal D	PEC2.19	Wei Shao-Hung	PEB1.34	
Van Heerwaarden C	PEC1.03	Vieira, A	PSC2.05	Wells-Bennik Marjon HJ	PEC2.55	
Van Herreweghe JM	PEB1.33	Viel A	PEB2.18	Wemmenhove E	PEC2.55	
van Hoek A	PED1.36	Viel Alessia	PEA1.32		PEC1.58	
van Hooijdonk ACM	PEC2.55	Vignolo Graciela	PEB2.42		PEC1.91	
Van Hulle SWH	PED1.25	Vigre H	PEC1.08	Werbrouck, Hadewig	PSB1.01	
Van Impe J	PEC1.63	Vihavainen E	PEA2.28	Wevers, E	PSB2.06	
Van Impe J	PEC1.85	Vihavainen EJ	PEA2.39	Whitehead K	PED2.16	
Van Impe J	PEC1.94	Vilela D	PEA1.59	Wieczorek K	PED1.13	
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Van Landschoot A	PEA2.31		PEA2.20	Wieczorek Kinga	PEB1.07	
Van Langenhove H	PEA2.11		PEA2.21	Wieczorek Kinga	PED1.12	
van Lieverloo JAM	PEC2.55		PEB2.31	Wijman J	PEB2.04	
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Van Loco Joris	PEC1.102		PED2.30	Wilches Pérez D	PED2.43	
Van Loco, J	PSB1.04		PED2.31		PED2.44	
van Melis C	PEB2.29		PSA2.04		PEC2.26	
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						Yang J-Y
						Yasui C
						Yavarmanesh Maso
						Yazdankhah S
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* PEE2.24 The effects of four selected synbiotics on community and activity of the intestinal microbiota using a simulated colon model

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Prebiotics and probiotics, used in combinations as synbiotics, are used to positively manipulate the intestinal microbiota. Prebiotics have previously been reported to stimulate probiotics in the gastro-intestinal tract. The aim of this work has been to investigate the synbiotic potential of *Lactobacillus acidophilus* NCFM in combination with raffinose, cellobiose, isomaltulose and hydrolysed beta-glucan, respectively.

The effect of the synbiotic combinations were investigated in a four stage semi-continuous colon model with mixed human fecal culture. Synthetic medium with either prebiotic (2%) and probiotic bacteria (2×10^9 CFU) or without synbiotic was fed to the system and after 48 hrs of simulated colonic fermentation samples were collected. Microbial genus and species densities were analyzed using quantitative PCR and volatile fatty acid concentrations were measured by GC-MS.

Apart from *L. acidophilus*, no significant changes were seen in the total microbial numbers. The tested synbiotics were meanwhile able to give a beneficial shift in the activity of the colonic microbes. Especially levels of the short chain fatty acids butyric and acetic acid were increased. The synbiotics were equally capable of decreasing the branched chain fatty acids but differences in the capability of increasing short chain fatty acids were observed. Isomaltulose and raffinose synbiotics increased the level of acetic acid most whilst cellobiose and raffinose synbiotics gave a larger increase in the levels of butyric acid. The synbiotic *L. acidophilus* NCFM and beta-glucan gave the highest levels of propionic acid. The results of this work show that the four synbiotic combinations tested have promising synbiotic potentials as they are able to increase levels of beneficial short chain fatty acids. However, human trials are needed to confirm these findings. Apart from conducting human trials with selected synbiotics, the synbiotics will be further investigated by differential proteomics to give more understanding of the interactions between the pre- and probiotics.

PEE2.25 Potential Title: Impact of polydextrose on biomarkers of gut health

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The biological and clinical importance of resident gastrointestinal microbiota is becoming increasingly recognised by consumers and healthcare workers. Although it is known that many disease states involve bacterial metabolism, the human gut microbiota may also be considered as extremely relevant for improvement to host health. The effects of prebiotics in altering the composition of the gut microbiota is well known, however the preliminary data from animal and human studies have indicated that they may also have an effect on the systemic and local immune system in the gut.

Polydextrose (PDX) is a soluble fibre synthesised from dextrose, it is frequently used to increase the non-dietary fibre content of food. Previous *in vitro* studies have shown that polydextrose is selectively fermented by the faecal microbiota and it may have activities against colorectal cancer.

In the present study, the impact of PDX on the human gut microbiota in a double-blind, placebo-controlled, crossover study with thirty-one healthy volunteers was investigated.

Changes within the gut microbiota composition were monitored using fluorescence *in situ* hybridization and PCR-DGGE. Gastrointestinal symptoms and stool characteristics were also recorded.

Additionally changes in the genotoxic nature of the faecal water of the volunteers were assessed to determine whether the intervention might offer potential benefits against bowel cancer. Levels of faecal bacteria in the *Clostridium histolyticum* and the lactobacilli/enterococci groups were lower following PDX treatment as compared to the placebo treatment. The DGGE profiles indicated that the bacterial profiles of the baseline and the placebo were significantly different, as was the placebo compared to the PDX treatment. Consumption of PDX also led to lowered genotoxicity levels as compared to the placebo. Furthermore a trend for less abdominal discomfort, less hard stool and reduced snacking were observed following PDX treatment.

In conclusion, this work demonstrated that PDX may improve gastrointestinal well being and offer potential benefits against bowel cancer risk markers.

PEE2.26 Effects of

colon ca

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Arabinoxylans are complex polysaccharides from reduced risk of cardiovascular disease in arabinoxylans treated rats, a mechanism of food intake in this study two strains of fraction without fermentation supernatants and steady state (SS) supernatants were tested to protect from hydrolysis. All tested fermentation HT29 cells from hydrolysis significantly reduced the growth. The ability of the 66% of ferulic acid by fermentation which did not cause